

Serial Number: 09/855,160

CRF Processing Date: 5/8/2001
Edited by: Ar
Verified by: Ar (STIC staff)**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 2,9 - aligned amino acid nos.

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,160

DATE: 05/08/2001
TIME: 12:24:53

Input Set : A:\49849.txt
Output Set: N:\CRF3\05082001\I830160.raw

**Does Not Comply
Corrected Diskette Needed**

4 <110> APPLICANT: YLIHONKO, Kristiina
5 TORKKELL, Sirke
6 PALMU, Kaisa
7 HAKALA, Juha
9 <120> TITLE OF INVENTION: GENE CLUSTER INVOLVED IN NOGALAMYCIN BIOSYNTHESIS,
10 AND ITS USE IN PRODUCTION OF HYBRID ANTIBIOTICS
12 <130> FILE REFERENCE: 1574/49849
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/830,160
C--> 14 <141> CURRENT FILING DATE: 2001-04-23
14 <150> PRIOR APPLICATION NUMBER: PCT/FI99/00870
15 <151> PRIOR FILING DATE: 1999-10-20
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

575 <210> SEQ ID NO: 2
576 <211> LENGTH: 342
577 <212> TYPE: PRT
578 <213> ORGANISM: Streptomyces nogalater ATCC 27451
580 <220> FEATURE:
581 <223> OTHER INFORMATION: "translate of snogI, function: aminotransferase"
583 <400> SEQUENCE: 2
585 Met Thr Val His Val Trp Asp Tyr Leu Pro Glu Tyr Glu Leu Glu Arg
586 1 5 10 15
588 Glu Asp Ile His Asp Ala Val Glu Thr Val Phe Arg Ser Gly Arg Leu
E--> 589 ~~20~~ 20 ~~25~~ 25 ~~30~~ 30
591 Val Leu Gly Glu Ser Val Arg Gly Phe Glu Ser Glu Phe Ala Ser Phe
E--> 592 35 40 45
594 Gln Gly Val Gly His Ala Val Gly Val Asp Asn Gly Thr Asn Ala Val
E--> 595 50 55 60
597 Lys Leu Gly Leu Gln Ala Leu Gly Val Gly Pro Gly Asp Glu Val Val
E--> 598 65 70 75 80
600 Thr Val Ser Asn Thr Ala Ala Pro Thr Val Val Ala Ile Asp Ser Ala
E--> 601 85 90 95
603 Gly Ala Thr Pro Val Phe Val Asp Val Arg Glu Glu Asp Tyr Leu Met
E--> 604 100 105 110
606 Asp Thr Ser Gln Val Glu Ala Val Leu Thr Pro Arg Thr Arg Cys Leu
E--> 607 115 120 125
609 Leu Pro Val His Leu Tyr Gly Gln Cys Val Asp Met Ala Pro Leu Arg
E--> 610 130 135 140
612 Asp Leu Ala Ala Arg His Asn Leu Val Ile Leu Glu Asp Cys Ala Gln
E--> 613 145 150 155 160
615 Ala His Gly Ala Arg Arg His Gly Arg Leu Ala Gly Ser Thr Gly Asp
E--> 616 165 170 175
618 Ala Ala Ala Phe Ser Phe Tyr Pro Thr Lys Val Leu Gly Ala Tyr Gly

misaligned nos.

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E--> 619          180          185          190
      621 Asp Gly Gly Ala Val Leu Thr Asp Asp Glu Arg Val Ala Asp Arg Leu
E--> 622          195          200          205
      624 Arg Arg Leu Arg Tyr Tyr Gly Met Glu Ser Arg Tyr Tyr Val Val Glu
E--> 625          210          215          220
      627 Thr Pro Gly His Asn Ser Arg Leu Asp Glu Val Gln Ala Glu Ile Leu
E--> 628 225          230          235          240
      630 Arg Arg Lys Leu Ser Arg Leu Pro Ser Tyr Ile Glu Ala Arg Arg Ala
E--> 631          245          250          255
      633 Val Ala Arg Arg Tyr Glu Glu Gly Leu Ala Asp Thr Gly Leu Leu Leu
E--> 634          260          265          270
      636 Pro Arg Thr Ala Gln Gly Asn Glu His Val Tyr Tyr Val Tyr Val Val
E--> 637          275          280          285
      639 Arg His Pro Arg Arg Asp Ala Val Leu Glu Ala Leu Arg Ala Ser Tyr
E--> 640          290          295          300
      642 Asp Ile Ala Leu Asn Ile Ser Tyr Pro Trp Pro Val His Thr Met Thr
E--> 643 305          310          315          320
      645 Gly Phe Ser His Leu Gly Tyr Ala Lys Gly Ser Leu Pro Val Thr Glu
E--> 646          325          330          335
      648 Ala Leu Ala Asp Glu Ile
E--> 649          340
      1091 <210> SEQ ID NO: 9
      1092 <211> LENGTH: 350
      1093 <212> TYPE: PRT
      1094 <213> ORGANISM: Streptomyces nogalater ATCC 27451
      1096 <220> FEATURE:
      1097 <223> OTHER INFORMATION: "translate of snogK, function: dTDP-glucose-4,6-dehydratase"
      1099 <400> SEQUENCE: 9
      1101 Met Ala Ser His Thr Ser Ala Thr Thr Asp Val Asn Ile Leu Val Thr
      1102 1          5          10          15
      1104 Gly Ala Val Gly Phe Ile Gly Ser Ala Tyr Val Arg Met Leu Leu Glu
E--> 1105          20          25          30
      1107 Asn Arg Ala Pro Gly Ala Gly Ala Pro Ala Val Arg Val Thr Val Leu
E--> 1108          35          40          45
      1110 Asp Lys Leu Thr Tyr Ala Gly Asn Leu Thr Asn Leu Asp Ala Val Arg
E--> 1111          50          55          60
      1113 Gly Asp Arg Leu Arg Phe Val Arg Gly Asp Ile Leu Asp Ala Glu Leu
E--> 1114 65          70          75          80
      1116 Val Asp Glu Leu Met Ala His Ser Asp Gln Val Val His Phe Ala Ala
E--> 1117          85          90          95
      1119 Glu Ser His Val Asp Arg Ser Ile Arg Ala Ala Asp Asp Phe Val Leu
E--> 1120          100          105          110
      1122 Thr Asn Val Val Gly Thr Gln Arg Leu Leu Asp Ala Ala Leu Arg His
E--> 1123          115          120          125
      1125 Gly Val Glu Pro Phe Val Leu Val Ser Thr Asp Glu Val Tyr Gly Ser
E--> 1126          130          135          140
      1128 Ile Ala Ser Gly Ser Trp Pro Glu Glu His Pro Leu Ser Pro Asn Ser
E--> 1129 145          150          155          160
      1131 Pro Tyr Ala Ala Ser Lys Ala Ser Ala Asp Leu Met Ala Phe Ala Cys

```

*same
env*

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```

E--> 1132          165          170          175
      1134 His Arg Thr His Gly Leu Asp Val Arg Val Thr Arg Cys Ser Asn Asn
E--> 1135          180          185          190
      1137 Tyr Gly Pro Arg Gln His Pro Glu Lys Leu Ile Pro Arg Phe Val Thr
E--> 1138          195          200          205
      1140 Asn Leu Leu Asp Gly Leu Pro Val Pro Leu Tyr Gly Asp Gly Arg Asn
E--> 1141          210          215          220
      1143 Val Arg Glu Trp Leu His Val Glu Asp His Cys Arg Gly Val Asp Leu
E--> 1144 225          230          235          240
      1146 Val Arg Thr Ala Gly Arg Pro Gly Gly Val Tyr His Ile Gly Gly Gly
E--> 1147          245          250          255
      1149 Arg Glu Leu Ser Asn Arg Glu Leu Val Gly Met Leu Leu Glu Leu Cys
E--> 1150          260          265          270
      1152 Gly Ala Asp Trp Ser Ser Val Arg His Val Pro Asp Arg Lys Gly His
E--> 1153          275          280          285
      1155 Asp Leu Arg Tyr Ser Leu Asp Trp Gly Arg Ala Arg Glu Glu Leu Gly
E--> 1156          290          295          300
      1158 Tyr Arg Pro Ala Arg Glu Phe Ser Ser Gly Leu Arg Ser Thr Val Gln
E--> 1159 305          310          315          320
      1161 Trp Tyr Arg Glu Asn Arg Ser Trp Trp Glu Pro Leu Lys Arg Gly Val
E--> 1162          325          330          335
      1164 Thr Ala Pro Gly Gly Thr Ser Thr Val Val Pro Gly Val Arg
E--> 1165          340          345          350

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,160

DATE: 05/08/2001

TIME: 12:24:54

Input Set : A:\49849.txt

Output Set: N:\CRF3\05082001\I830160.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:589 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:1105 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9